



227274078.ST25.txt
SEQUENCE LISTING

<110> Lang, Jas C.

<120> Detecting the Expression of the DESC1 Gene in Squamous Cell Carcinoma

<130> 22727/04078

B1 <140> 09/674,035

<141> 2000-12-11

<150> PCT/IB99/01818

<151> 1999-11-11

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 1269

<212> DNA

<213> DESC1

<220>

<221> CDS

<222> (1)..(1269)

<223>

<400> 1

atg tat cgg cca gat gtg gtg agg gct agg aaa aga gtt tgt tgg gaa 48
Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
1 5 10 15

ccc tgg gtt atc ggc ctc gtc atc ttc ata tcc ctg att gtc ctg gca 96
Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala
Page 1

20

25

30

gtg	tgc	att	gga	ctc	act	gtt	cat	tat	gtg	aga	tat	aat	caa	aag	aag	144
Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	Asn	Gln	Lys	Lys	
		35					40					45				
acc	tac	aat	tac	tat	agc	aca	ttg	tca	ttt	aca	act	gac	aaa	cta	tat	192
Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	Thr	Asp	Lys	Leu	Tyr	
	50					55					60					
gct	gag	ttt	ggc	aga	gag	gct	tct	aac	aat	ttt	aca	gaa	atg	agc	cag	240
Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	Phe	Thr	Glu	Met	Ser	Gln	
65					70					75					80	
aga	ctt	gaa	tca	atg	gtg	aaa	aat	gca	ttt	tat	aaa	tct	cca	tta	agg	288
Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	Phe	Tyr	Lys	Ser	Pro	Leu	Arg	
				85					90					95		
B1 gaa	gaa	ttt	gtc	aag	tct	cag	gtt	atc	aag	ttc	agt	caa	cag	aag	cat	336
Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	
			100					105					110			
gga	gtg	ttg	gct	cat	atg	ctg	ttg	att	tgt	aga	ttt	cac	tct	act	gag	384
Gly	Val	Leu	Ala	His	Met	Leu	Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	
		115					120					125				
gat	cct	gaa	act	gta	gat	aaa	att	gtt	caa	ctt	gtt	tta	cat	gaa	aag	432
Asp	Pro	Glu	Thr	Val	Asp	Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	
	130					135					140					
ctg	caa	gat	gct	gta	gga	ccc	cct	aaa	gta	gat	cct	cac	tca	gtt	aaa	480
Leu	Gln	Asp	Ala	Val	Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	
145					150					155					160	
att	aaa	aaa	atc	aac	aag	aca	gaa	aca	gac	agc	tat	cta	aac	cat	tgc	528
Ile	Lys	Lys	Ile	Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	
				165					170					175		
tgc	gga	aca	cga	aga	agt	aaa	act	cta	ggg	cag	agt	ctc	agg	atc	gtt	576
Cys	Gly	Thr	Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	
			180					185					190			
ggg	ggg	aca	gaa	gta	gaa	gag	ggg	gaa	tgg	ccc	tgg	cag	gct	agc	ctg	624
Gly	Gly	Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	
		195					200					205				
cag	tgg	gat	ggg	agt	cat	gcg	tgt	gga	gca	acc	tta	att	aat	gcc	aca	672
Gln	Trp	Asp	Gly	Ser	His	Ala	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	
	210					215					220					
tgg	ctt	gtg	agt	gct	gct	cac	tgt	ttt	aca	aca	tat	aag	aac	cct	gcc	720
Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	Ala	
225					230					235					240	
aga	tgg	act	gct	tcc	ttt	gga	gta	aca	ata	aaa	cct	tcg	aaa	atg	aaa	768
Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	Met	Lys	
				245					250					255		
cgg	ggg	ctc	cgg	aga	ata	att	gtc	cat	gaa	aaa	tac	aaa	cac	cca	tca	816
Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	His	Pro	Ser	
			260					265					270			
cat	gac	tat	gat	att	tct	ctt	gca	gag	ctt	tct	agc	cct	gtt	ccc	tac	864

227274078.ST25.txt

His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr	
275 280 285	
aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt	912
Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe	
290 295 300	
caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat	960
Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn	
305 310 315 320	
gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata	1008
Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile	
325 330 335	
gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act	1056
Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr	
340 345 350	
cct aga atc tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc	1104
Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys	
355 360 365	
cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc	1152
Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile	
370 375 380	
tgg tac ctt gct gga ata gtg agc tgg gga gat gaa tgt gcg aaa ccc	1200
Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro	
385 390 395 400	
aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att	1248
Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile	
405 410 415	
act tca aaa act ggt atc taa	1269
Thr Ser Lys Thr Gly Ile	
420	

<210> 2

<211> 422

<212> PRT

<213> DESC1

<400> 2

Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
1 5 10 15

Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala
20 25 30

Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
35 40 45

227274078.ST25.txt

Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
50 55 60

Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
65 70 75 80

Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
85 90 95

Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
100 105 110

Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
115 120 125

Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
130 135 140

B1

Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
145 150 155 160

Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
165 170 175

Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
180 185 190

Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
195 200 205

Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
210 215 220

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
225 230 235 240

Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
245 250 255

Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
260 265 270

His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
275 280 285

Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
290 295 300

Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
305 310 315 320

Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
325 330 335

Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
340 345 350

Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
355 360 365

B1

Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
370 375 380

Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
385 390 395 400

Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
405 410 415

Thr Ser Lys Thr Gly Ile
420

<210> 3

<211> 1269

<212> DNA

<213> DESC1

<220>

<221> CDS

<222> (1)..(1269)

<223>

<400> 3

atg	tat	cgg	cca	gat	gtg	gtg	agg	gct	agg	aaa	aga	gtt	tgt	tgg	gaa	48
Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys	Trp	Glu	
1				5				10					15			

ccc	tgg	gtt	atc	ggc	ctc	gtc	atg	ttc	ata	tcc	ctg	att	gtc	ctg	gca	96
Pro	Trp	Val	Ile	Gly	Leu	Val	Met	Phe	Ile	Ser	Leu	Ile	Val	Leu	Ala	
			20					25					30			

227274078.ST25.txt

gtg tgc att gga gtc act gtt cat tat gtg aga tat aat caa aag aag Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys	144
acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr	192
gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln	240
aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg	288
gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His	336
B1 gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu	384
gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys	432
ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys	480
att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys	528
tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val	576
ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu	624
cag tgg gat ggg agt cat cgc tgt gga gca acc tta att aat gcc aca Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr	672
tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala	720
aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys	768
cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser	816
cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr	864

227274078.ST25.txt

aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt 912
 Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
 290 295 300

caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat 960
 Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
 305 310 315 320

gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata 1008
 Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
 325 330 335

gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act 1056
 Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
 340 345 350

cct aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc 1104
 Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
 355 360 365

cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc 1152
 Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
 370 375 380

tgg tac ctt gct gga ata gtg agc tcg gga gat gaa tgt gcg aaa ccc 1200
 Trp Tyr Leu Ala Gly Ile Val Ser Ser Gly Asp Glu Cys Ala Lys Pro
 385 390 395 400

aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att 1248
 Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
 405 410 415

act tca aaa act ggt atc taa 1269
 Thr Ser Lys Thr Gly Ile
 420

<210> 4

<211> 422

<212> PRT

<213> DESC1

<400> 4

Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
 1 5 10 15

Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala
 20 25 30

Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
 35 40 45

Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
 Page 7

50

55

60

Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
65 70 75 80

Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
85 90 95

Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
100 105 110

Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
115 120 125

Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
130 135 140

Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
145 150 155 160

Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
165 170 175

Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
180 185 190

Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
195 200 205

Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
210 215 220

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
225 230 235 240

Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
245 250 255

Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
260 265 270

His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
275 280 285

Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
290 295 300

Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
305 310 315 320

Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
325 330 335

Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
340 345 350

Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
355 360 365

Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
370 375 380

Trp Tyr Leu Ala Gly Ile Val Ser Ser Gly Asp Glu Cys Ala Lys Pro
385 390 395 400

Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
405 410 415

Thr Ser Lys Thr Gly Ile
420

<210> 5

<211> 28

<212> DNA

<213> D11 primer

<400> 5

tgcatcaagc aaacagttta ttgagatc

28

<210> 6

<211> 25

<212> DNA

<213> D10 primer

<400> 6

cctgttcctt acacaaathc agtac

25

<210> 7

<211> 28

<212> DNA

<213> D12 primer

<400> 7

tgacttgat gtagacctcg accttcag

28

<210> 8

<211> 22

<212> DNA

<213> D18 primer

B1 <400> 8

ggaatagtga gctcgggaga tg

22

<210> 9

<211> 28

<212> DNA

<213> D3 primer

<400> 9

tcactgttca ttatgtgaga tataatca

28

<210> 10

<211> 27

<212> DNA

<213> D4 primer

<400> 10

caccattgat tcaagtctct ggctcat

27